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P#5 OIPE

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/802,741A

DATE: 09/18/2001

TIME: 14:26:59

Input Set : N:\Crif3\RULE60\09802741A.txt

Output Set: N:\CRF3\09182001\I802741A.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Fisher, Douglas A.  
6 Gooding, Doug  
7 Streeter, Dave

C--> 9 (ii) TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE

11 (iii) NUMBER OF SEQUENCES: 14

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
15 (B) STREET: 3174 Porter Dr.  
16 (C) CITY: Palo Alto  
17 (D) STATE: CA  
18 (E) COUNTRY: USA  
19 (F) ZIP: 94304

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette  
23 (B) COMPUTER: IBM Compatible  
24 (C) OPERATING SYSTEM: DOS  
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/802,741A

C--> 29 (B) FILING DATE: 08-Mar-2001

35 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/987,466  
34 (B) FILING DATE: 29-January-1999

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Billings, Lucy J.  
39 (B) REGISTRATION NUMBER: 36,749  
40 (C) REFERENCE/DOCKET NUMBER: PF-0442 US

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 650-855-0555  
44 (B) TELEFAX: 650-845-4166

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 593 amino acids  
51 (B) TYPE: amino acid  
52 (C) STRANDEDNESS: single  
53 (D) TOPOLOGY: linear

55 (vii) IMMEDIATE SOURCE:

56 (A) LIBRARY: PROSN06  
57 (B) CLONE: 828228

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp  
63 1 5 10 15  
64 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser  
65 20 25 30

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```

66 Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
67      35                      40                      45
68 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
69      50                      55                      60
70 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
71      65                      70                      75                      80
72 Val Ala Ile Lys Gln Leu Ser Ala Gly Val Glu Asp Lys Arg Thr Thr
73      85                      90                      95
74 Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg Arg Val Val
75      100                     105                     110
76 Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser Gly Gln Val
77      115                     120                     125
78 Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu Gly Gln Arg
79      130                     135                     140
80 Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
81      145                     150                     155                     160
82 Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
83      165                     170                     175
84 Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly
85      180                     185                     190
86 Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met
87      195                     200                     205
88 Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys
89      210                     215                     220
90 Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val
91      225                     230                     235                     240
92 Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu
93      245                     250                     255
94 Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu
95      260                     265                     270
96 Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe
97      275                     280                     285
98 Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp
99      290                     295                     300
100 Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val
101      305                     310                     315                     320
102 Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys
103      325                     330                     335
104 Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
105      340                     345                     350
106 Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
107      355                     360                     365
108 Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
109      370                     375                     380
110 His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
111      385                     390                     395                     400
112 Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
113      405                     410                     415
114 Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met

```

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```

115           420           425           430
116 Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
117           435           440           445
118 His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
119           450           455           460
120 Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
121           465           470           475           480
122 Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu
123           485           490           495
124 Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala
125           500           505           510
126 Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val
127           515           520           525
128 Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp
129           530           535           540
130 Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met
131           545           550           555           560
132 Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu
133           565           570           575
134 Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys
135           580           585           590
136 Ala
137

```

140 (2) INFORMATION FOR SEQ ID NO: 2:

142 (i) SEQUENCE CHARACTERISTICS:

143 (A) LENGTH: 1997 base pairs

144 (B) TYPE: nucleic acid

145 (C) STRANDEDNESS: single

146 (D) TOPOLOGY: linear

148 (vii) IMMEDIATE SOURCE:

149 (A) LIBRARY: PROSN0T06

150 (B) CLONE: 828228

152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

154 GCTCCCCGCG GCGGCTGGCG TCGGGAAAGT ACAGTAAAAA GTCCGAGTGC AGCCGCCGGG      60
155 CGCAGGATGG GATCCGGCTC CTCCAGCTAC CGGCCAAGG CCATCTACCT GGACATCGAT      120
156 GGACGCATTC AGAAGGTAAT CTTAGCAAG TACTGCAACT CCAGCGACAT CATGGACCTG      180
157 TTCTGCATCG CCACCGGCCT GCCTCGGAAC ACGACCATCT CCCTGCTGAC CACCGACGAC      240
158 GCCATGGTCT CCATCGACCC CACCATGCCC GCGAATTCAG AACGCACTCC GTACAAAGTG      300
159 AGACCTGTGG CCATCAAGCA ACTCTCCGCT GGTGTGAGG ACAAGAGAAC CACAAGCCGT      360
160 GGCCAGTCTG CTGAGAGACC ACTGAGGGAC AGACGGGTTG TGGGCCTGGA GCAGCCCCGG      420
161 AGGGAAGGAG CATTTGAAAG TGGACAGGTA GAGCCCAGGC CCAGAGAGCC CCAGGGCTGC      480
162 TACCAGGAAG GCCAGCGCAT CCCTCCAGAG AGAGAAGAAT TAATCCAGAG CGTGCTGGCG      540
163 CAGGTTGCAG AGCAGTTCTC AAGAGCATTC AAAATCAATG AACTGAAAGC TGAAGTTGCA      600
164 AATCACTTGG CTGTCTTAGA GAAACGCGTG GAATTGGAAG GACTAAAAGT GGTGGAGATT      660
165 GAGAAATGCA AGAGTGACAT TAAGAAGATG AGGGAGGAGC TGGCGGCCAG AAGCAGCAGG      720
166 ACCAACTGCC CCTGTAAGTA CAGTTTTTTG GATAACCACA AGAAGTTGAC TCCTCGACGC      780
167 GATGTTCCCA CTTACCCCAA GTACCTGCTC TCTCCAGAGA CCATCGAGGC CCTGCGGAAG      840
168 CCGACCTTTG ACGTCTGGCT TTGGGAGCCC AATGAGATGC TGAGCTGCCT GGAGCACATG      900
169 TACCACGACC TCGGGCTGGT CAGGGACTTC AGCATCAACC CTGTCACCCT CAGGAGGTGG      960
170 CTGTTCTGTG TCCACGACAA CTACAGAAAC AACCCCTTCC ACAACTTCCG GCACTGCTTC      1020

```

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```

171 TGCCTGGCCC AGATGATGTA CAGCATGGTC TGGCTCTGCA GTCTCCAGGA GAAGTTCTCA 1080
172 CAAACGGATA TCCTGATCCT AATGACAGCG GCCATCTGCC ACGATCTGGA CCATCCCGGC 1140
173 TACAACAACA CGTACCAGAT CAATGCCCCG ACAGAGCTGG CGGTCCGCTA CAATGACATC 1200
174 TCACCGCTGG AGAACCACCA CTGCGCCGTG GCCTTCCAGA TCCTCGCCGA GCCTGAGTGC 1260
175 AACATCTTCT CCAACATCCC ACCTGATGGG TTCAAGCAGA TCCGACAGGG AATGATCACA 1320
176 TTAATCTTGG CCACTGACAT GGCAAGACAT GCAGAAATTA TGGATTCTTT CAAAGAGAAA 1380
177 ATGGAGAATT TTGACTACAG CAACGAGGAG CACATGACCC TGCTGAAGAT GATTTTGATA 1440
178 AAATGCTGTG ATATCTCTAA CGAGGTCCGT CCAATGGAAG TCGCAGAGCC TTGGGTGGAC 1500
179 TGTTTATTAG AGGAATATTT TATGCAGAGC GACCGTGAGA AGTCAGAAGG CCTTCCTGTG 1560
180 GCACCGTTCA TGGACCGAGA CAAAGTGACC AAGGCCACAG CCCAGATTGG GTTCATCAAG 1620
181 TTTGTCTGA TCCCAATGTT TGAAACAGTG ACCAAGCTCT TCCCCATGGT TGAGGAGATC 1680
182 ATGCTGCAGC CACTTTGGGA ATCCCAGAT CGCTACGAGG AGCTGAAGCG GATAGATGAC 1740
183 GCCATGAAAG AGTTACAGAA GAAGACTGAC AGCTTGACGT CTGGGGCCAC CGAGAAGTCC 1800
184 AGAGAGAGAA GCAGAGATGT GAAAAACAGT GAAGGAGACT GTGCCTGAGG AAAGCGGGGG 1860
185 GCGTGGCTGC AGTTCTGGAC GGGCTGGCCG AGCTGCGCGG GATCCTTGTG CAGGGAAGAG 1920
186 CTGCCCTGGG CACCTGGCAC CACAAGACCA TGTTTCTAA GAACCATTTT GTTCACTGAT 1980
187 ACAAAAAAAAA AAAAAAA
1997

```

189 (2) INFORMATION FOR SEQ ID NO: 3:

191 (i) SEQUENCE CHARACTERISTICS:

192 (A) LENGTH: 713 amino acids

193 (B) TYPE: amino acid

194 (C) STRANDEDNESS: single

195 (D) TOPOLOGY: linear

197 (vii) IMMEDIATE SOURCE:

198 (A) LIBRARY: THP1PLB02

199 (B) CLONE: 156196

201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

203 Leu Ala Cys Phe Leu Asp Lys His His Asp Ile Ile Ile Ile Asp His
204 1 5 10 15
205 Arg Asn Pro Arg Gln Leu Asp Ala Glu Ala Leu Cys Arg Ser Ile Arg
206 20 25 30
207 Ser Ser Lys Leu Ser Glu Asn Thr Val Ile Val Gly Val Val Arg Arg
208 35 40 45
209 Val Asp Arg Glu Glu Leu Ser Val Met Pro Phe Ile Ser Ala Gly Phe
210 50 55 60
211 Thr Arg Arg Tyr Val Glu Asn Pro Asn Ile Met Ala Cys Tyr Asn Glu
212 65 70 75 80
213 Leu Leu Gln Leu Glu Phe Gly Glu Val Arg Ser Gln Leu Lys Leu Arg
214 85 90 95
215 Ala Cys Asn Ser Val Phe Thr Ala Leu Glu Asn Ser Glu Asp Ala Ile
216 100 105 110
217 Glu Ile Thr Ser Glu Asp Arg Phe Ile Gln Tyr Ala Asn Pro Ala Phe
218 115 120 125
219 Glu Thr Thr Met Gly Tyr Gln Ser Gly Glu Leu Ile Gly Lys Glu Leu
220 130 135 140
221 Gly Glu Val Pro Ile Asn Glu Lys Lys Ala Asp Leu Leu Asp Thr Ile
222 145 150 155 160
223 Asn Ser Cys Ile Arg Ile Gly Lys Glu Trp Gln Gly Ile Tyr Tyr Ala
224 165 170 175

```

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```

225 Lys Lys Lys Asn Gly Asp Asn Ile Gln Gln Asn Val Lys Ile Ile Pro
226      180      185      190
227 Val Ile Gly Gln Gly Gly Lys Ile Arg His Tyr Val Ser Ile Ile Arg
228      195      200      205
229 Val Cys Asn Gly Asn Asn Lys Ala Glu Lys Ile Ser Glu Cys Val Gln
230      210      215      220
231 Ser Asp Thr Arg Thr Asp Asn Gln Thr Gly Lys His Lys Asp Arg Arg
232 225      230      235      240
233 Lys Gly Ser Leu Asp Val Lys Ala Val Ala Ser Arg Ala Thr Glu Val
234      245      250      255
235 Ser Ser Gln Arg Arg His Ser Ser Met Ala Arg Ile His Ser Met Thr
236      260      265      270
237 Ile Glu Ala Pro Ile Thr Lys Val Ile Asn Val Ile Asn Ala Ala Gln
238      275      280      285
239 Glu Ser Ser Pro Met Pro Val Thr Glu Ala Leu Asp Arg Val Leu Glu
240      290      295      300
241 Ile Leu Arg Thr Thr Glu Leu Tyr Ser Pro Gln Phe Gly Ala Lys Asp
242 305      310      315      320
243 Asp Asp Pro His Ala Asn Asp Leu Val Gly Gly Leu Met Ser Asp Gly
244      325      330      335
245 Leu Arg Arg Leu Ser Gly Asn Glu Tyr Val Leu Ser Thr Lys Asn Thr
246      340      345      350
247 Gln Met Val Ser Ser Asn Ile Ile Thr Pro Ile Ser Leu Asp Asp Val
248      355      360      365
249 Pro Pro Arg Ile Ala Arg Ala Met Glu Asn Glu Glu Tyr Trp Asp Phe
250      370      375      380
251 Asp Ile Phe Glu Leu Glu Ala Ala Thr His Asn Arg Pro Leu Ile Tyr
252 385      390      395      400
253 Leu Gly Leu Lys Met Phe Ala Arg Phe Gly Ile Cys Glu Phe Leu His
254      405      410      415
255 Cys Ser Glu Ser Thr Leu Arg Ser Trp Leu Gln Ile Ile Glu Ala Asn
256      420      425      430
257 Tyr His Ser Ser Asn Pro Tyr His Asn Ser Thr His Ser Ala Asp Val
258      435      440      445
259 Leu His Ala Thr Ala Tyr Phe Leu Ser Lys Glu Arg Ile Lys Glu Thr
260      450      455      460
261 Leu Asp Pro Ile Asp Glu Val Ala Ala Leu Ile Ala Ala Thr Ile His
262 465      470      475      480
263 Asp Val Asp His Pro Gly Arg Thr Asn Ser Phe Leu Cys Asn Ala Gly
264      485      490      495
265 Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His
266      500      505      510
267 His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn
268      515      520      525
269 Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly
270      530      535      540
271 Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His
272 545      550      555      560
273 Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu

```

VERIFICATION SUMMARY

DATE: 09/18/2001

PATENT APPLICATION: US/09/802,741A

TIME: 14:27:00

Input Set : N:\Crf3\RULE60\09802741A.txt

Output Set: N:\CRF3\09182001\I802741A.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]